



1	MDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSAN	50
1	PPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSAN	48
51	YSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPF	100
49	YSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPF	98
101	VCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLK	150
99	VCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLK	148
151	IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAK	200
149	IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAK	198
201	TWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPR	250
199	TWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPR	248
251	EGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV	300
249	EGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV	298
301	HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNC	350
299		348
351	VEDKMLSTVAVLTLG 365	
349	VEDKMLSTVAVLTLG 363	

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1	MDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC	42
51	PGLGGAGALDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC	100
43	SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL	92
01	SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL	150
93	THTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT	142
51	THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT	200
43	FKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ	192
201	FKKHQQLKIHQCQNTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ	250
93	KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE	242
	KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE	300
243	RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ	292
301	RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ	350
93	SLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLC	342
351	SLTRHAVVHDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLC .	400
343	QNGESPNCVEDKMLSTVAVLTLG 365	
01	QNGESPNCVEDKMLSTVAVLTLG 423	

21	PGLGGAGALDPPAVVAESVSSLTIADAFTAAGESSAPTPPRPALPRRFTC	100
1		40
101	SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL	150
41	SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL	90
151	THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT	200
91	THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT	140
201	FKKHQQLKIHQCQNTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ	250
141	FKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ	190
251	KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKOHMKTHAPE	300
191	KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE	240
301	RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ	350
241	RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ	290
351	SLTRHAVVHDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLC	400
291	SLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLC	340
401	QNGESPNCVEDKMLSTVAVLTLG 423	
341		

1	CCGCCGGCCGTGGTCGCCGACGCCCGACGCCCCGCCGCCGCCGCCGCCGCCGCC	50 17
51 18	GTTCATTGCAGCCGGGGGGGGGGGGGGGGGGGGGGGGGG	100 34
101 35	TTCCCAGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGC PRRFICSFPDCSANYS	150 50
151	AAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGACC	200
51	K A W K L D A H L C K H T G E R P	67
201	ATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTACC	250
68	F V C D Y E G C G K A F I R D Y H	84
251 85	ATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTTTGTTT	300 100
301	GCAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAA	350
101	A A N G C D Q K F N T K S N L K K	117
351	ACATTTTGAACGCAAACATGAAAAATCAACAAAAACAATATATGCAGTT	400
118	H F E R K H E N Q Q K Q Y I C S F	134
401	TTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCAT	450
135	E D C K K T F K K H Q Q L K I H	150
451 151	CAGTGCCAGCATACCAATGAACCTCTATTCAAGTGTACCCAGGAAGGA	500 167
501	TGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCC	550
168	G K H F A S P S K L K R H A K A H	184
551	ACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGG	600
185	E G Y V C Q K G C S F V A K T W	200
601	ACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATG	650
201	T E L L K H V R E T H K E E I L C	217

651 218	TGAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACA EVCRKTFKRKDYLKQHM	700 234
701 235	TGAAAACTCATGCCCCAGAAAGGGATGTATGTCGCTGTCCAAGAGAAGGC K T H A P E R D V C R C P R E G	750 250
751 251	TGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATCCTCTC C G R T Y T T V F N L Q S H I L S	800 267
801 268	CTTCCATGAGGAAAGCCGCCCTTTTGTGTGTGAACATGCTGGCTG	850 284
851 285	AAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGAT T F A M K Q S L T R H A V V H D	900 300
901 301	CCTGACAAGAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAACG P D K K K M K L K V K K S R E K R	950 317
951 318	GAGTTTGGCCTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAG S L A S H L S G Y I P P K R K Q G	1000 334
1001 335	GGCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGTGTGGAAQQG LS LCQNGESPNCVE	1050 350
1051 351	GACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAAGAACTGCA D K M L S T V A V L T L G *	1100 364
1101	CTGCTTTGTTTAAAGGACTGCAGACCAAGGAGCGAGCTTTCTCTCAGAGC	1150
1151	ATGCTTTTCTTTATTAAAATTAC 1173	

 $(x,y) = (x,y)^{\frac{1}{2}} \cdot (x,y)^{\frac{1}{2}}$ 

M R S S G A D A G R C 51 GCCTGGTGACCGCGCGCGCTCCCGGAAGTGTGCCGGCGTCGCGCGAAGGT 100 L V T A R A P G S V P A S R E G 101 TCAGCAGGAGCCGTGGGCCGGGCGCGCGTTCCCGGCACGTGTCTCGGC 150 S A G S R G P G A R F P A R V S A ACGTGGCAGCGCCTGGCCCTGGGCTTGGAGGCGCCCGGCCCCTGGATC R G S A P G P G L G G A G A L D P CGCCGGCCGTGGTCGCCGAGTCGGTGTCCTTGACCATCGCCGACGCG 201 P A V V A E S V S S L T I A D A TTCATTGCAGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCGCCCCGCGCT FIAAGESSAPTPPRPAL 94 301 TCCCAGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCA 350 P R R F I C S F P D C S A N Y S K AAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGACCA AWKLDAHLCKHTGERP 401 TTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTACCA 450 F V C D Y E G C G K A F I R D Y H 500 LSRHILTHTGEKPFVCA CAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAA 501 550 ANGCDQKFNTKSNLKK 551 CATTTGAACGCAAACATGAAAATCAACAAAAACAATATATGCAGTTT 178 H F E R K H E N O O K O Y I C S F 601 TGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCATC 650 EDCKKTFKKHQQLKIHQ 700 CQNTNEPLFKCTQEGC 227

701 GGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCA 750 228 G K H F A S P S K L K R H A K A H 751 CGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGA 800 245 EGYVCQKGCSFVAKTWT 801 CGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGT 850 ELLKHVRETHKEEILC 262 851 GAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACAT 900 278 E V C R K T F K R K D Y L K Q H M 901 GAAAACTCATGCCCCAGAAAGGGATGTATGTCGCTGTCCAAGAGAAGGCT 950 KTHAPERDVCRCPREGC 311 295 951 GTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATCCTCTCC 1000 G R T Y T T V F N L Q S H I L S 327 1050 328 F H E E S R. P F V C E H A G C G K 1051 AACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATC 1100 345 T F A M K Q S L T R H A V V H D P 1101 CTGACAAGAAGAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAACGG 1150 D K K K M K L K V K K S R E K R 377 362 1151 GAGTTTGGCCTCTCATCTCAGTGGATATATCCTCCCAAAAGGAAACAAGG 1200 378 E F G L S S Q W I Y P P K R K Q G 1201 GCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGTGTGGAAG 1250 Q G L S L C Q N G E S P N C V E D 395 411, 1251 ACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAAGAACTGCAC 1300 412 K M L S T V A V L T L G  $\star$ 424 1301 TGCTTTGTTTAAAGGACTGCAGACCAAGGAGTCGAGCTTTCTCTCAGAGC 1350

FIGURE 5

1399